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In the Claims:

Please amend claims 1 – 5, 10, 12 – 16, 18, 22 – 26, 28, 30 – 33, 36, 38 – 39, 42, 44 – 48, 51, 53 – 55, 57, 59, 61 and 65 – 66 as follows:

1. (Five Times Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a cotton fiber transcriptional initiation region [factor] functional in a cotton fiber cell and an open reading frame encoding a protein in a pigment biosynthesis pathway, wherein said transcriptional initiation region [factor] is selected from the group consisting of:
 - a. nucleotides 65-4163 of SEQ ID NO: 7, and
 - b. SEQ ID NO: 15[, and
 - c. a DNA sequence which hybridizes with SEQ ID NO: 15 under conditions comprising hybridization in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and washing in 2X SSC, 0.1% SDS at 42 ° C for 3 X 30 minutes].
2. (amended) The DNA sequence according to Claim 1, further comprising a [transport signal encoding] sequence encoding a transit peptide from a plant nuclear-encoded gene.
3. (twice amended) The DNA sequence according to Claim 2, wherein said [transport signal encoding sequence comprises] transit peptide is a plastid transit peptide.
4. (twice amended) The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a [transport signal encoding] sequence encoding a transit peptide from a signal peptide which provides for transport across the rough endoplasmic reticulum.

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5. (amended) The DNA sequence according to Claim 4, wherein said DNA sequence further comprises as an operably joined component, 3' to said open reading frame, a sequence encoding a vacuolar [localization] targeting signal.
6. (Reiterated) The DNA sequence of Claim 1 wherein said pigment is melanin or indigo.
7. (Reiterated) The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.
8. (Reiterated) The DNA sequence of Claim 7 wherein said gene is selected from the group consisting of ORF438, *tyrA*, anthocyanin R gene, anthocyanin C1 gene, *pig*, and *tna*.
9. (Reiterated) A DNA construct comprising a DNA sequence of Claim 1.
10. (twice amended) A DNA construct comprising [two] a first and a second DNA sequence[s] according to Claim 1, wherein the open reading frame of said first DNA sequence encodes a different gene than the open reading frame of said second DNA sequence.[said protein in a biosynthesis pathway in each of said two DNA sequences is not encoded by the same gene.]
12. (amended) A plant cell comprising [a] the DNA construct of Claim 9.
13. (amended) A plant comprising [a] the cell of Claim 12.
14. (three times amended) A method of modifying fiber phenotype in a cotton plant, said method comprising:

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transforming a plant cell with [a] the DNA construct according to Claim 9 or 10;
and

[growing] regenerating a plant comprising fiber tissue from said plant cell [to produce a plant comprising fiber tissue], wherein said fiber tissue comprises a substrate of said protein in a pigment biosynthesis pathway, and wherein said protein reacts with said substrate to produce said pigment, whereby the phenotype of said fiber is modified.

15. (twice amended) The method of Claim 14 wherein said DNA construct further comprises a [transport signal encoding] sequence encoding a transit peptide from a plant nuclear-encoded gene.
16. (twice amended) The method of Claim 14 wherein said DNA construct further comprises a [transport signal encoding] sequence encoding a transit peptide, which encodes a signal peptide which provides for transport across the rough endoplasmic reticulum.
18. (twice amended) The method of Claim 16 wherein said plant cell is further transformed with a second DNA construct according to Claim 9 or 10 and wherein the open reading frame of the DNA sequence from the first DNA construct encodes a different gene than the open reading frame of the second DNA construct. [DNA comprises constructs for expression of two proteins in a pigment biosynthesis pathway wherein said two proteins are not encoded by the same gene.]
19. (Reiterated) The method of Claim 18 wherein said pigment is melanin and said proteins are encoded by *tyrA* and ORF438.
20. (Reiterated) The method of Claim 18 wherein said pigment is indigo and said proteins are encoded by *tna* and *pig*.

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21. (Reiterated) The method of Claim 18 wherein said pigment is anthocyanin and said two proteins are the anthocyanin R and C1 proteins.
22. (twice amended) The method of Claim 14 wherein said fiber tissue is obtained from a cotton burr.
23. (twice amended) A recombinant DNA construct comprising [the cotton tissue transcriptional sequence shown in] nucleotides 65 – 4163 of SEQ ID NO: 7.
24. (twice amended) A recombinant DNA construct comprising [the cotton tissue transcriptional sequence shown in] SEQ ID NO: 15.
25. (twice amended) An isolated DNA sequence comprising the [nucleotide] sequence shown in SEQ ID NO: 1.
26. (twice amended) An isolated DNA sequence comprising the [nucleotide] sequence shown in SEQ ID NO: 12.
28. (twice amended) The DNA sequence according to Claim 1, wherein said transcriptional initiation region [factor] is obtained by [the method of] probing a genomic library derived from a plant fiber tissue.
30. (amended) The DNA sequence according to Claim 59, further comprising a [transport signal encoding] sequence encoding a transit peptide from a plant nuclear-encoded gene.
31. (amended) The DNA sequence according to Claim 30, wherein said [transport signal encoding sequence comprises] transit peptide is a plastid transit peptide.

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32. (amended) The DNA sequence according to Claim 59, further comprising a [transport signal encoding sequence for a signal peptide] sequence encoding a transit peptide which provides for transport across the rough endoplasmic reticulum.
33. (amended) The DNA sequence according to Claim 32, wherein said sequence further comprises, 3' to said open reading frame, a sequence encoding a vacuolar [localization] targeting signal.
34. (Reiterated) The DNA sequence of Claim 57 wherein said open reading frame is from a bacterial gene.
35. (Reiterated) The DNA sequence of Claim 34 wherein said bacterial gene is selected from the group consisting of ORF438, *tyrA*, *pig* and *tna*.
36. (amended) A DNA construct comprising [a] the DNA sequence of Claim 59.
37. (Reiterated) The DNA construct of Claim 36 wherein said cotton plant cell is a cotton fiber cell.
38. (amended) A plant cell comprising [a] the DNA construct of Claim 36.
39. (amended) A plant comprising [a] the plant cell of Claim 38.
42. (three times amended) The DNA sequence according to Claim 59 wherein said transcriptional initiation region [factor] is obtained by [the method of] probing a genomic library derived from a plant fiber tissue.
44. (four times amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region [factor]

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functional in a cotton plant cell and an open reading frame encoding an enzyme in a biosynthetic pathway of melanin or indigo, wherein said transcriptional initiation region [factor] is selected from the group consisting of:

- a. nucleotides 65-4163 of SEQ ID NO: 7, and
- b. SEQ ID NO: 15[, and
- c. a DNA sequence which hybridizes with SEQ ID NO: 15 under conditions comprising hybridization in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and washing in 2X SSC, 0.1% SDS at 42 ° C for 3 X 30 minutes].

45. (amended) The DNA sequence according to Claim 44, further comprising a [transport signal encoding] sequence encoding a transit peptide from a plant nuclear-encoded gene.

46. (amended) The DNA sequence according to Claim 45, wherein said [transport signal encoding sequence comprises] transit peptide is a plastid transit peptide.

47. (amended) The DNA sequence according to Claim 44, further comprising a [transport signal encoding] sequence encoding a transit peptide [for a signal peptide] which provides for transport across the rough endoplasmic reticulum.

48. (amended) The DNA sequence according to Claim 47, wherein said sequence further comprises, 3'to said open reading frame, a sequence encoding vacuolar [localization] targeting signal.

49. (Reiterated) The DNA sequence of Claim 44 wherein said open reading frame is from a bacterial gene.

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50. (Reiterated) The DNA sequence of Claim 49 wherein said bacterial gene is selected from the group consisting of ORF438, *tyrA*, *pig*, and *tna*.

51. (amended) The DNA construct comprising [a] the DNA sequence of Claim 44.

52. (Reiterated) The DNA construct of Claim 51 wherein said cotton plant cell is a cotton fiber cell.

53. (amended) A plant cell comprising [a] the DNA construct of Claim 51.

54. (amended) A plant comprising [a] the plant cell of Claim 53.

55. (twice amended) The DNA sequence according to Claim 44 wherein said transcriptional initiation region [factor] is obtained by probing a genomic library derived from a plant fiber tissue.

57. (four times amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region [factor] functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional initiation region [factor] is selected from the group consisting of:

- a. nucleotides 65-4163 of SEQ ID NO: 7, and
- b. SEQ ID NO: 15[, and
- c. a DNA sequence which hybridizes with SEQ ID NO: 15 under conditions comprising hybridization in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and washing in 2X SSD, 0.1% SDS at 42 ° C for 3 X 30 minutes].

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59. (three times amended) A DNA sequence comprising a transcriptional initiation region [factor] functional in a cotton plant cell, wherein said transcriptional initiation region [factor] is selected from the group consisting of:
- a) nucleotides 65-4163 of SEQ ID NO: 7, and
 - b) SEQ ID NO: 15[, and
 - c) a DNA sequence which hybridizes with up to the full length of SEQ ID NO: 15 under conditions comprising hybridization in a solution comprising 50% formamide, 5X SSD, 0.1% SDS, 5mM EDTA, 10X Denhardt's solution, and 25mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and washing in 2X SSC, 0.1% SDS at 42 ° C for 3 X 30 minutes].
61. (amended) A recombinant DNA construct comprising [the cotton tissue transcriptional sequence shown in] nucleotides 57 – 4155 of SEQ ID NO: 11.
65. (amended) An isolated DNA sequence comprising [the cotton transcriptional sequence shown in] nucleotides 65 – 4163 of SEQ ID NO: 7.
66. (amended) An isolated DNA sequence comprising [the cotton transcriptional sequence shown in] SEQ ID NO: 15.

Please add the following new claims:

67. (New) An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 2.
68. (New) An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 13.

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